

EXHIBIT 6

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DeCypher Results for Job: Smith-Waterman Similarity Search

Results by Query

Click on a query below to view its search results.

[1394_PTH9903](#)

Search Details

Results for: 1394_PTH9903; (Length=669/QuerySize=669)

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Maximum possible score for this scoring matrix and query: 6690.00

RANK	SCORES	QF	TARGET LOCUS NAME	ACCESSION#	TF	TARGET
P_SCORE	DESCRIPTION					
1	3455.00	C	gi 1787371 gb AE000213.1 AE00021	AE000213.1	D	
ecoli_ae	-1.0e+00		Escherichia coli K12 MG1655 section 103 of 400 of th			
2	246.00	D	gi 1787371 gb AE000213.1 AE00021	AE000213.1	D	
ecoli_ae	-1.0e+00		Escherichia coli K12 MG1655 section 103 of 400 of th			

RANK 1 Score = 3455.00 P_Score = -1.0e+00
Q = CGI_3078ws206512.seq QF = C #Q Symbols = 669
T = gi|1787371|gb|AE000213.1|AE00021 TF = D #T Symbols = 10959
A = AE000213.1
D = Escherichia coli K12 MG1655 section 103 of 400 of the complete genome

Identical Match = 500 Similar = 500 Total # Of Gaps = 4

Identity: Alignment = 75% Query = 74% Target = 4%

Similarity: Alignment = 75% Query = 74% Target = 4%

QS = 662 QE = 1 TS = 8606 TE = 9268

Q 662 TCCTT-AGGGGTAACATCCCGCCATTCCCCGTTGCCAGCGAGTCAGCGTATAGCTGCC
TCCTT A GT AC TC CGCCATTC CC TT GC AG TCCA G TA CC
T 8606 TCCTTAATCTGTCACTTCTGCCATTGCCATTGGCAAGATTATCCAAAGAGTAATCACC

Q 603 CATGGCGTAGCGAATGAGTCGCAGGGTAGGGAAGCCCACATGCGCAGTCATGCGCCTGAC

CAT GC TAGCGAAT AGTCGAG GT GGGAGCC ACATG GC GTCATGCG C AC
 T 8666 CATCGCATAGCGAATCAGTCGAGCGTGGGAAGCCAACATGGCGGTATGCGCGC

 Q 543 CTGTCGGTTGCGGCCTTCATAAAGGGTGATTTAAGCCAGCTGGTAGGAATGGATTTACG
 CTG CG TT CG CCTTCATA A GGTGAT TT AGCCAGCTGGT GGAAT TTT CG
 T 8726 CTGGCGATTACGTCTTCATATAAGGTGATCTCAGCCAGCTGGTGGGAATACTTTGCG

 Q 483 CTCACGAATCGCGGGTTGCGCGGCCACAGCCACTCGGGTCATTACACGTTCAATACC
 TCACGAAT GG GG TT CGCGCCA A CCAC CGGGTTC T AC G TC CC
 T 8786 TTCACGAATTGGTGGATTCCCGCGGCCATAACCACGCGGGTCGTCAACCAGCTCCGCGCC

 Q 423 AGCCGGCAGGGTGGGACCGTCGTTCAGCGTTACGCCGTTGCAC--GCTTGCCAGCGAC
 GC GGCAGGGT GG CC TC TT A GTTACGCC TTGCGCA GCTT GCG C
 T 8846 GGCAGGGCAGGGTAGGGCCATCTTAAGGTTACGCCATTGCGCAAGGCTCAAGTGC

 Q 365 GCGTCGTCCGGCTCGCCTCAACCTGCACATAGTAAATTTCCGGTACGTTGCCCGGC
 GT GT GG CCTTC ACCTGCACATA TA ATTTTCCGGT CGTT CCCGGC
 T 8906 TTGT-GT-GGAAATACCTTCCACCTGCACATAATAGATTTCCGGTGC

 Q 305 TGAGTAAGCCTGGCCTGGAGCACGCCGTATTGTAAGGACCAGCAGCCCCTCGCTGTC
 TG GT A C GCCTG A C CGCCGT ATTGGT AG ACCAGCA CCC TCGCT TCG
 T 8964 TGGGTTAAACGCGCCTGCAACGCGCCGTATTGGTCAGCACCAGCAACCCTCGCTATCG

 Q 245 CGATCCAGACGTCCCCTGCGTAGACTCCCTGTACGGGATAAAGTCCTTCAGCGTGCTG
 CG TC AG CG CC GCTGC TA AC CCCTG AC GGGAT AA TC TT A GT TG
 T 9024 CGGTCAAGGCACCTGCTGCATAAACACCCCTGAACCGGGATGAATTCTTAATGTTTG

 Q 185 CGCCCGGCCTCGTGGTAAACTGCGGAATACATCGTAGGGTTATTGAACAGTATGACC
 CG CCGGC TC TCGGT AACTGCGG A ACATCGTAGGGTTATTGAACAG AT AC
 T 9084 CGTCCGGCTTCATCGGTGAACTGCGGAAGAACATCGTAGGGTTATTGAACAGGATCACA

 Q 125 CGCGTTGGCTGGGTTCTGGCGTTCTTCTGGTGGCTTGTGAGCTGAATCGCTCAACC
 CGCGT GGCTGG TTC GG T C CTGGT G GT G GAGCTGAATCGCT AAC
 T 9144 CGCGTGGCTGGTTTCAGGTTACGCCCTGGTAGAACGTTGCGAGCTGAATCGCTTAACC

 Q 65 CGGTGTTTCTAAAAGAAGTTTCGTATGGTATTTCAGGCGTTATCAATTGCCGCATT
 GGTG TTTCTAAAAGAAGTTT CATGGTATTTCAG TTAT AATTGCCGCATT
 T 9204 TGGTGATTTCTAAAAGAAGTTTGCATGGTATTTCAGAGATTATGAATTGCCGCATT

 Q 5 ATAGC
 ATAGC
 T 9264 ATAGC

RANK 2 Score = 246.00 P_Score = -1.0e+00
 Q = CGI_3078ws206512.seq QF = D #Q Symbols = 669
 T = gi|1787371|gb|AE000213.1|AE00021 TF = D #T Symbols = 10959
 A = AE000213.1
 D = Escherichia coli K12 MG1655 section 103 of 400 of the complete
 genome
 Identical Match = 197 Similar = 197 Total # Of Gaps = 22
 Identity: Alignment = 52% Query = 29% Target = 1%
 Similarity: Alignment = 52% Query = 29% Target = 1%
 QS = 234 QE = 570 TS = 10054 TE = 10387

```

Q      234 ACGTCTGGATCGCGACAGCGAGGGGCTGCTGGCCTTACCAATGACGGCGTGCCTCAGGC
      ACGTCTGG TCG G CAGCGA G T C G TT C AA GA CGTG C G
T      10054 ACGTCTGGTCGTG-CAGCGATCGAATAC--GCAATTGCTAACGA--TCGTGACTCTG--
Q      294 CAGGCTTACTCAGCCGGCAAACGTACCGGAA--AAATTTAC--TATGTGCAGGTTGAAG
      T ACTC G G CAAA G A C A AA TT AC A G GC G TT AAG
T      10107 -----TGACTCTGGTGCACAAAGGCAACATCATGAAGTTACCGAAGGAGC-GTTTAAAG
Q      350 GCGAGCCGGACGACGCGTCGCTGGCAAAGCTGCGAACGGCGTAACGCTGAACGACGGTC
      C G AC A G CGC G A AG T G CGG G A CTGA CGACGGT
T      10161 ACTGGGCTACCAAGCTGGCGCGTGAAGAGTTGG---CGGTGAA---CTGATCGACGGTG
Q      410 CCACCCCTGCCGGCTGGTATTGAACCGTGTGAATGAACCCGAGTGGCTGTGGCCGGCAACC
      C CC TG C TGAA GT T AA AACCCGA C TGGC G A C
T      10215 GC-CCGTGGC-----TGAAAGT-TAAA--AACCCGA---ACACTGGCAAAGAGATC
Q      470 CGCCGATT----CGTGAGCGTAAATCCATTCC--ACCAG-----CTGGCTT
      C ATT CGTGA G AT CATTCC A CAG C GGCT
T      10259 GTC--ATTAAGACGTGATTGCTGATGCATTCTGCAACAGATCCTGCTGCGTCCGGCTG
Q      511 AAAATCA-----CCCTTATGAAGGCCGCAAC----CGACAGGTCAAGCG-CATGAC
      AA AT A CCT TATGAA CC AAC C ACA TC G CG C TG C
T      10317 AATATGATGTTATGCCGTATGAA--CCTGAACGGTGAACATTTCTGACGCCCTGGC
Q      558 TGCATGTGGC
      GCGCA GT GGC
T      10375 AGCGCAGGTTGGC

```

Job Details

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[BEGIN JOB STATUS]

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[END SEARCH TIME] Fri Dec 06 12:44:24 2002
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[EXTEND PENALTY] -5
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[QUERY TYPE] NT

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[TARGET SET] d:\decypher\target\ecoli_ae000213.txt
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[MAX ALIGNMENTS] 20
[THRESHOLD] 1
[ALIGNMENT THRESHOLD] 20
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[OUTPUT FORMAT] TEXT MAXSCORE PERCENTAGE EXTRACTALIGNED MATCHCHARACTER
[OUTPUT FORMAT] HTML WEB
[CGI REFERING PAGE] http://tblast-m.genomecorp.com/algo-sw/sw_nn.shtml
[CGI COOKIE] Set-Cookie: DeCypher=; expires=Saturday, 06-Dec-03
12:00:00 GMT; path=/; domain=tblast-m.genomecorp.com;

[JOB MESSAGES]

[END JOB STATUS]

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For assistance contact
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